(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
4 October 2001 (04.10.2001)

PCT

(10) International Publication Number
WO 01/073134 A3

(51) International Patent Classification[7]: C12Q 1/68

(21) International Application Number: PCT/US01/09993

(22) International Filing Date: 28 March 2001 (28.03.2001)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/192,700 28 March 2000 (28.03.2000) US

(71) Applicant *(for all designated States except US)*: **THE GOVERNMENT OF THE UNITED STATES OF AMERICA, as represented by THE SECRETARY, DEPARTMENT OF HEALTH & HUMAN SERVICES, THE NATIONAL INSTITUTES OF HEALTH** [US/US]; Office Of Technology Transfer, 6011 Executive Boulevard, Suite #325, Rockville, MD 20852 (US).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: **WANG, Ena** [CN/US]; 4500 Gretna Street, Bethesda, MD 20814 (US). **MARINCOLA, Francesco, M.** [US/US]; 10110 Chapel Road, Potomac, MD 20854 (US). **MILLER, Lance, D.** [US/US]; 13109-E Millhaven Place, Germantown, MD 20874 (US).

(74) Agent: NOONAN, William, D.; Klarquist Sparkman,LLP, One World Trade Center, Suite 1600, 121 SW Salmon Street, Portland, Oregon 97204 (US).

(81) Designated States *(national)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States *(regional)*: ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:
— *with international search report*

(88) Date of publication of the international search report:
16 January 2003

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 01/073134 A3

(54) Title: GENE PROFILING ARRAYS

(57) Abstract: Ordered arrays of mixtures of nucleic acid molecules are provided, which mixtures reflect the expression profile of one or more specimens, such as different cells or tissues. In particular embodiments, complete mRNA mixtures from specimens are separately arrayed on a substrate. Specimens from which such mixtures of nucleic acid molecules are produced can be taken from any source, including animal, plant and/or microbial cells, and can be assembled in any collection desired. The collections can, for instance, include different cell types, different phenotypes, cells grown under different conditions, cells of different ages or developmental stages, and so forth. The nucleic acid arrays are provided in both macro- and microarray formats, and are suitable for gene profiling in which relative quantitative expression from a single source or multiple sources may be determined. Techniques are also disclosed for producing high-fidelity, amplified mixtures of nucleic acid molecules using a combination of anti-sense RNA amplification and template-switching synthesis. Amplified mixtures produced using this method can, for instance, be applied to the disclosed arrays. The disclosed arrays allow high throughput analysis of differential gene expression in a specimen (such as a tumor) or a variety of specimens (such as a variety of tumors), and are suitable for automated preparation and analysis.

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 01/09993

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)
WPI Data, PAJ, EPO-Internal, MEDLINE, BIOSIS, EMBASE, CHEM ABS Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	ZHAO N ET AL: "High-density cDNA filter analysis: a novel approach for large-scale, quantitative analysis of gene expression" GENE, ELSEVIER BIOMEDICAL PRESS. AMSTERDAM, NL, vol. 156, no. 2, 1995, pages 207-213, XP004042356 ISSN: 0378-1119	1-15, 30-42, 44-57, 59-72
Y	see whole doc.	16-29, 43,58

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[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

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Date of the actual completion of the international search	Date of mailing of the international search report
30 August 2002	18/09/2002

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL – 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Mueller, F

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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication,where appropriate, of the relevant passages	Relevant to claim No.
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